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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Levy, Gary
- (ii) TITLE OF INVENTION: Methods of Modulating Immune Coagulation
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: BERESKIN & PARR
  - (B) STREET: 40 King Street West
  - (C) CITY: Toronto
  - (D) STATE: Ontario
  - (E) COUNTRY: Canada
  - (F) ZIP: M5H 3Y3
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Gravelle, Micheline
  - (B) REGISTRATION NUMBER: 40,261
  - (C) REFERENCE/DOCKET NUMBER: 9579-006
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (416) 364-7311
  - (B) TELEFAX: (416) 361-1398

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4630 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TCTTCCTGTG	CGTTTCTAAA	ACTTGTGATG	CAAACGCTCC	CACCCTTTCC	TGGGAACACA	1260
GAAAGCCTGA	CTCAGGCCAT	GGCCGCTATT	AAAGCAGCTC	CAGCCCTGCG	CACTCCCTGC	1320
TGGGGTGAGC	AGCACTGTAA	AGATGAAGCT	GGCTAACTGG	TACTGGCTGA	GCTCAGCTGT	1380
TCTTGCCACT	TACGGTTTTT	TGGTTGTGGC	AAACAATGAA	ACAGAGGAAA	TTAAAGATGA	1440
AAGAGCAAAG	GATGTCTGCC	CAGTGAGACT	AGAAAGCAGA	GGGAAATGCG	AAGAGGCAGG	1500
GGAGTGCCCC	TACCAGGTAA	GCCTGCCCCC	CTTGACTATT	CAGCTCCCGA	AGCAATTCAG	1560
CAGGATCGAG	GAGGTGTTCA	AAGAAGTCCA	AAACCTCAAG	GAAATCGTAA	ATAGTCTAAA	1620
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CTTTAAGCCA TAAATCACTC TGTTCATTCC TCCAGGTATT CGTTATCTAA TAGGGCAATT	3180
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ATGCTGTTAT CCAATGAACA CTTGCAAGCA ATTAGCAATA TTGAGAATTA TACATTAGAT	3360
TTACAATTCT TTTAATTTCT ATTGAAACTT TTTCTATTGC TTGTATTACT TGCTGTATTT	3420
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GGTTCCTCAGA CTAAGGGAAC TAATATCTAT ATAATTAAAC TTGTTTCAATTT ATCATTCATG	4020
AAATATAAAA TACTTGTCAT TTAAACCGTT TAAAAATGTG GTAGCATAAT GTCACCCCAA	4080
AAAGCATTCA GAAAGCAATG TAACTGTGAA GACCAGGGTT TAAAGGTAAT TCATTTATAG	4140
TTTATAACTC CTTAGATGTT TGATGTTGAA AACTGCTTTA ACATGAAAAT TATCTTCCTC	4200
TGCTCTGTGT GAACAATAGC TTTTAATTTA AGATTGCTCA CTACTGTACT AGACTACTGG	4260
TAGGTTTTTTT TGGGGGGGGG TGGGTAGGGA TATGTGGGTA ATGAAGCATT TACTTACAGG	4320

(2) INFORMATION FOR SEQ ID NO:2:

(A) LENGTH: 439 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Tyr	Gly	Phe	Leu 20	Val	Val	Ala	Asn	Asn 25	Glu	Thr	Glu	Glu	Ile 30	Lys	Asp
Glu	Arg	Ala 35	Lys	Asp	Val	Cys	Pro 40	Val	Arg	Leu	Glu	Ser 45	Arg	Gly	Lys
Cys	Glu 50	Glu	Ala	Gly	Glu	Cys 55	Pro	Tyr	Gln	Val	Ser 60	Leu	Pro	Pro	Leu
Thr 65	Ile	Gln	Leu	Pro	Lys 70	Gln	Phe	Ser	Arg	Ile 75	Glu	Glu	Val	Phe	Lys 80
Glu	Val	Gln	Asn	Leu 85	Lys	Glu	Ile	Val	Asn 90	Ser	Leu	Lys	Lys	Ser 95	Cys
Gln	Asp	Cys	Lys 100	Leu	Gln	Ala	Asp	Asp 105	Asn	Gly	Asp	Pro	Gly 110	Arg	Asn
Gly	Leu	Leu 115	Leu	Pro	Ser	Thr	Gly 120	Ala	Pro	Gly	Glu	Val 125	Gly	Asp	Asn
Arg	Val 130	Arg	Glu	Leu	Glu	Ser 135	Glu	Val	Asn	Lys	Leu 140	Ser	Ser	Glu	Leu
Lys 145	Asn	Ala	Lys	Glu	Glu 150	Ile	Asn	Val	Leu	His 155	Gly	Arg	Leu	Glu	Lys 160
Leu	Asn	Leu	Val	Asn 165	Met	Asn	Asn	Ile	Glu 170	Asn	Tyr	Val	Asp	Ser 175	Lys
Val	Ala	Asn	Leu 180	Thr	Phe	Val	Val	Asn 185	Ser	Leu	Asp	Gly	Lys 190	Cys	Ser
Lys	Cys	Pro 195	Ser	Gln	Glu	Gln	Ile 200	Gln	Ser	Arg	Pro	Val 205	Gln	His	Leu
Ile	Tyr 210	Lys	Asp	Cys	Ser	Asp 215	Tyr	Tyr	Ala	Ile	Gly 220	Lys	Arg	Ser	Ser

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Glu Thr Tyr Arg Val Thr Pro Asp Pro Lys Asn Ser Ser Phe Glu Val  
 225 230 235 240  
 Tyr Cys Asp Met Glu Thr Met Gly Gly Gly Trp Thr Val Leu Gln Ala  
 245 250 255  
 Arg Leu Asp Gly Ser Thr Asn Phe Thr Arg Thr Trp Gln Asp Tyr Lys  
 260 265 270  
 Ala Gly Phe Gly Asn Leu Arg Arg Glu Phe Trp Leu Gly Asn Asp Lys  
 275 280 285  
 Ile His Leu Leu Thr Lys Ser Lys Glu Met Ile Leu Arg Ile Asp Leu  
 290 295 300  
 Glu Asp Phe Asn Gly Val Glu Leu Tyr Ala Leu Tyr Asp Gln Phe Tyr  
 305 310 315 320  
 Val Ala Asn Glu Phe Leu Lys Tyr Arg Leu His Val Gly Asn Tyr Asn  
 325 330 335  
 Gly Thr Ala Gly Asp Ala Leu Arg Phe Asn Lys His Tyr Asn His Asp  
 340 345 350  
 Leu Lys Phe Phe Thr Thr Pro Asp Lys Asp Asn Asp Arg Tyr Pro Ser  
 355 360 365  
 Gly Asn Cys Gly Leu Tyr Tyr Ser Ser Gly Trp Trp Phe Asp Ala Cys  
 370 375 380  
 Leu Ser Ala Asn Leu Asn Gly Lys Tyr Tyr His Gln Lys Tyr Arg Gly  
 385 390 395 400  
 Val Arg Asn Gly Ile Phe Trp Gly Thr Trp Pro Gly Val Ser Glu Ala  
 405 410 415  
 His Pro Gly Gly Tyr Lys Ser Ser Phe Lys Glu Ala Lys Met Met Ile  
 420 425 430  
 Arg Pro Lys His Phe Lys Pro  
 435

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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 AAATATGAGA ACTGGACATG GTGGTACACA CCTGTGATCT CTGTGTTTAG GAGGGAGAGG 360

CAGAGAGATC AGGAGTTCAA GGCCAGCCTG AGCTACTTGA GACCCAGTCT AAATAAATAA 420  
GAGATAGATT ACAGAGTGCC TTAACTAGT ACAGAGAAAG AATTTGGGTT TATCTGTGTC 480  
AGTTACGCTG AAATAATTTT TAAGTAATAA AATCCCTTTT AATAAGAAAC CTTATGAGGT 540  
CAGTATGCAC AATGAACTTA AGAGAGACCC CCAGCTCCTG AGCTGAGTGA TGGGGAAGGA 600  
CAGCCACTGC CTGTGATGTG TGAGTGACGT GCTTCCAAGT GTTTTAACCA CTGACGATTA 660  
CATAGCCTGC ACAGTCAGGA GAAAACAGCC GTATTCTCTG CCAGTTCTCT TCCCTTTTAC 720  
AAACAGATGA GAGACACACA CAGAGAATCC ATTTAAAGAG CGGACCTTTG TTCTGATTAG 780  
GGGCAATTTT AAGTACTTAA GAGTTCACAC AAAGTCTAGC CTTCAAAAAG AAAACAGGTT 840  
CCCAAACCTAG GGAGGAAACA GAATCATTTT CATTTTGGTG ACATTTAGTG GGAAGAAGCT 900  
CACAGACATT TAGACGTTCC AACTCTTTCC CCACTAGTGG ACCAAGTATA TAATATGGTA 960  
TCTTTTGGGC ACTGGTATTA CAACTGTTTT TTAAACAAAA GACTTTCCTT GTGCTTTACT 1020  
AAAAACCCAG ACGGTGAATC TTGAATACAA TGCGTGGCAC CCACGGCAGG CATTCTATTG 1080  
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 ATT 5403

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

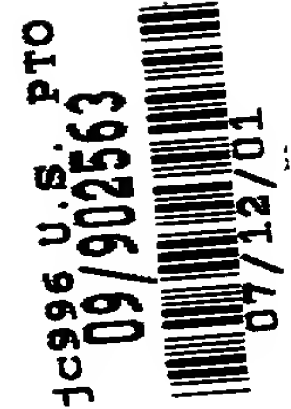
## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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 35 40 45  
 Glu Gly Ser Gln Cys Pro Phe Gln Leu Thr Leu Pro Thr Leu Thr Ile  
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SEQUENCE LISTING



<110> Levy, Gary

<120> Methods of Modulating Immune Coagulation

<130> 9579-37

<140>

<141>

<150> US 09/442,143

<151> 1999-11-15

<160> 53

<170> PatentIn version 3.1

<210> 1

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<212> DNA

<213> Homo sapiens

<400> 1

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cacggcaggc attctattgt gcatagtttt gactgacagg agatgacagc atttggctgc 180  
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21

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20